In the specification:

Please replace the previously amended paragraph on page 8, lines 22-27, of the specification with the following currently amended paragraph.

> Fig. 1 shows the sequence alignment of previously known bacterial RNase P protein subunits using the ClustalW alignment program (Thompson et al., Nucleic Acids Research 22: 4673, 1994) and the alignment of the RNase P sequences of the present invention (SEQ ID NOs: 39-~~95~~ 91).

Please replace the paragraph on page 9, lines 1-23, of the specification with the following amended paragraph.

> Figs. 2A-2S shows the nucleic acid sequences (SEQ ID NOs 1-19) encoding the amino acid sequences (SEQ ID NOs 20-38) of the bacterial RNase P polypeptides of the invention. The nucleic acid and amino acid sequences were derived from the following pathogenic bacterial species: *Streptococcus mutans* (Fig. 2A; SEQ ID NOs: 1 and ~~18~~ 20, respectively); *Klebsiella pneumoniae* (Fig. 2B; SEQ ID NOs: 2 and ~~19~~ 21, respectively); *Salmonella paratyphi* A (Fig. 2C; SEQ ID NOs: 3 and ~~20~~ 22, respectively); *Pseudomonas aeruginosa* (Fig. 2D; SEQ ID NOs: 4 and ~~21~~ 23, respectively); *Corynebacterium diphtheriae* (Fig. 2E; SEQ ID NOs: 5 and ~~22~~ 24, respectively); *Chlamydia trachomatis* (Fig. 2F; SEQ ID NOs: 6 and ~~23~~ 25, respectively); *Vibrio cholerae* Serotype 01, Biotype El Tor, Strain N16961 (Fig. 2G; SEQ ID NOs: 7 and ~~24~~ 26, respectively); *Neisseria gonorrhoea* FA 1090 (Fig. 2H; SEQ ID NOs: 8 and ~~25~~ 27, respectively); *Neisseria meningitidis* Serogroup A, Strain Z2491 (Fig. 2I; SEQ ID NOs: 9 and ~~26~~ 28, respectively); *Streptococcus pyogenes* M1 (Fig. 2J; SEQ ID NOs: 10 and ~~27~~ 29, respectively); *Bordetella pertussis* Tohama I (Fig. 2K; SEQ ID NOs: 11 and ~~28~~ 30, respectively); *Porphyromonas gingivalis* W83 (Fig. 2L; SEQ ID NOs: 12 and ~~29~~ 31, respectively); *Streptococcus pneumoniae* Type 4 (Fig. 2M; SEQ ID NOs: 13 and ~~30~~ 32, respectively); *Clostridium difficile* 630 (Fig. 2N; SEQ ID NOs: 14 and ~~31~~ 33, respectively); *Camphylobacter jejuni* NCTC (Fig. 2O; SEQ ID NOs: 15 and ~~32~~ 34, respectively); *Bacillus anthracis* Ames (Fig. 2P; SEQ ID NOs: 16 and ~~33~~ 35, respectively); *Mycobacterium avium* 104 (Fig. 2Q; SEQ ID NOs: 17 and ~~34~~ 36, respectively); *Staphylococcus aureus* NCTC

8325 (Fig. 2R; SEQ ID NOs: 18 and ~~35~~ 37, respectively); and *Staplylococcus aureus* COL (Fig. 2S; SEQ ID NOs: 19 and ~~36~~ 38, respectively).

Please replace the paragraph on page 22, lines 10-21, of the specification with the following amended paragraph.

The preferred reaction buffer contains 50 mM Tris-HCl (pH 7.5), 100 mM ammonium chloride and 10 mM magnesium chloride. Concentrations of 10-100 mM, 25-500 mM and 1-100 mM of the above, respectively, can be substituted, as can other buffering agents such as MOPS or HEPES, or other monovalent cations, such as sodium or potassium. When the assay is run in either 96 ~~98~~ or 384-well polystyrene or polypropylene assay plates, there is a very significant decrease in the fluorescence intensity and polarization of the annealed substrate over time in the absence of enzyme. Various conditions have been tested to prevent the loss of signal with time. The preferred conditions include addition of 10-40 µg/ml carbonic anhydrase and 10-100 µg/ml polyC to the buffer. Other materials, such as, 0.5-5% glycerol, 10-100 µg/ml hen egg lysozyme, 10-50 µg/mL tRNA, 1-10 mM DTT, or 2-10 mM DTT can also be added to the buffer to prevent some loss of signal.

Kindly replace the Sequence Listing filed on January 10, 2003, with the amended Sequence Listing, submitted herewith.